AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Draft Genome Sequence of *Klebsiella pneumoniae* KGM-IMP216 Harboring $bla_{CTX-M-15}$, bla_{DHA-1}, bla_{TEM-1B}, bla_{NDM-1}, bla_{SHV-28}, and bla_{OXA-1}, Isolated from a Patient in Lebanon

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We present the draft genome of highly drug-resistant *Klebsiella pneumoniae* KGM-IMP216, isolated from a urine sample collected from a patient in Lebanon. The draft genome sequence consisted of 77 contigs, including a combined 5,731,500 bases with 57% G+C content.

Received 27 November 2015 **Accepted** 7 December 2015 **Published** 28 January 2016

Citation Tokajian S, Eisen JA, Jospin G, Matar G, Araj GF, Coil DA. 2016. Draft genome sequence of *Klebsiella pneumoniae* KGM-IMP216 harboring $bla_{CTX-M-15}$, bla_{DHA-1}, bla_{TEM-1B}, bla_{NDM-1}, bla_{SHV-28}, and bla_{OXA-1}, isolated from a patient in Lebanon. Genome Announc 4(1):e01632-15. doi:10.1128/genomeA.01632-15.

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Klebsiella pneumoniae is among the most important causes of both hospital and community-acquired serious bacterial infections in humans. Extended-spectrum β-lactamase (ESBL)–producing organisms remain important causes of the failure of therapy with cephalosporins and have serious infection-control consequences. Infections due to ESBL-producing *K. pneumoniae* are most often involved in urinary and respiratory tract infections (1). The ESBL genes are mostly plasmid-encoded (2), and most ESBLs can be divided into three genotypes: TEM, SHV, and CTX-M (3). The emergence of ESBL-producing bacteria is now a critical concern. β-lactamases are able to hydrolyze oxyiminocephalosporins and aztreonam, and constitute an increasingly important mechanism of antimicrobial resistance among nosocomial Gram-negative pathogens (4). ESBLs of the CTX-M type, with CTX-M-15 being the variant most commonly identified in species of human origin, and the plasmid-encoded AmpC-type β-lactamases (bla_{DHA}) have been recognized to be of growing importance (5). Carbapenems are the primary therapeutic agents for infections caused by ESBLs. The extensive use of carbapenems led to the emergence of isolates with resistance genes coding for carbapenemases (6). Among the clinically significant carbapenemases are class B (NDM-1: New Delhi metallo-β-lactamase-1) and class D (OXA-1) (7).

In this study we sequenced *K. pneumoniae* KGM-IMP216 of multilocus sequence type ST-14 harboring $bla_{CTX-M-15}$, bla_{DHA-1}, bla_{TEM-1B}, bla_{NDM-1}, bla_{SHV-28}, and bla_{OXA-1}, isolated from a urine sample at the American University of Beirut Medical Center in Lebanon (8–10).

A Nextera XT kit (Illumina, San Diego, CA, USA) was used to simultaneously fragment and adapter-tag the library, as per the manufacturer's instructions. The library was normalized by bead-based affinity and then sequenced using the MiSeq version 3 600-cycle kit (Illumina) to perform 300-bp paired-end sequencing on a MiSeq instrument (Illumina), per the manufacturer's instructions. Quality trimming and error correction of the reads resulted in 4,192,299 high-quality reads. All sequence processing and assembly was performed using the A5-miseq assembly pipeline. This pipeline automates the processes of data cleaning, error correction, contig assembly, scaffolding, and quality control (11, 12). The initial assembly produced 77 contigs, for which no scaffolding was obtained. The final collection of contigs was submitted to GenBank. The final draft genome sequence consisted of a combined 5,731,500 bases with 57% G+C content. Automated annotation was performed using the RAST annotation server (13). *K. pneumoniae* KGM-IMP216 contains 5,499 predicted coding sequences and 112 predicted RNAs. Moreover, IncN, IncL/M, IncFII(K), IncFIA(HI1), IncR, and IncFIB(K) plasmid types were detected using the PlasmidFinder version 1.3 web server (https://cge.cbs.dtu.dk/services/PlasmidFinder) (14).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LJOI00000000. The version described in this paper is the first version, LJOI01000000.

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